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Meiosis, the master driver of gene duplication in higher plants?

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ABSTRACT

Meiosis is a critical biological process for reproduction and genetic variation in higher plants. Gene duplication is a prominent feature of plant genomic architecture. Meiosis and gene duplication are of fundamental importance in unraveling the nature of genetics and evolution. The ideas and findings in this letter demonstrate a highly significant connection between meiosis and gene duplication, bring together these two disparate fields of study and highlight the importance of meiosis for understanding the evolutionary success of flowering plants. These insights and opinions open a new area of investigation and point to a significant way to illustrate the impact of duplicated genes on meiosis and fitness in higher plants, as well as their ultimate evolutionary, ecological, and agronomic impacts in light of challenges that have arisen due to global climate change. This study addresses novel ideas and viewpoints in plant developmental genomics and evolution.

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1. Introduction

Gene duplication is a common and abundant event in plants; on average, 65% of annotated genes in plant genomes have a duplicate copy [1]. Gene duplication remains of specific interest because of both the abundance of duplicate genes in plants and their potential to contribute to plant evolution in nature [2–5]. Angiosperms (flowering plants) are of particular interest for studying the impact of gene duplication on plant reproduction and evolution in nature (e.g., Upland cotton in this study, $2n = 4X = 52$, 2.5 Gb). Compared to mammalian and most other plant genomes, angiosperms undergo gene duplication events more frequently [6,7]. It is unknown what major selective forces are associated with plant genome-wide gene duplication. The biological processes to which gene duplication primarily contributes during growth and development in plants is a vitally important question, the answer to which will indicate the major evolutionary force for gene duplication.

2. Results and discussion

Reproduction is pivotal for plant survival and for the evolution of life in nature. We are now beginning to understand which life cycle stage and which duplicate genes have dominantly

contributed to reproductive evolution in plants at the genome scale. Interestingly, transcriptome analysis in our study showed that the expression of genome-wide duplicated genes during the stage of meiosis (close to 50%) was significantly higher than that during the stages of pollen development and vegetative growth (both less than 20%) (Fig. 1). Our data unequivocally presented increase in the expression of genome-wide duplicated genes in the stage of meiosis but not in the stage of mature pollen development.

Our findings suggest that meiosis, the key stage of plant reproduction, is the major associated selective force for gene duplication during plant evolution. Moreover, the duplicate genes overrepresented during meiosis in our study are annotated and predominantly enriched in critical pathways of plant hormone signal transduction (Fig. 2). This finding is consistent with the gene balance hypothesis, which suggests that the expression levels of duplicate genes encoding members of the components of signal transduction pathways need to be maintained for correct function [8]. Meiosis occurring during male gametogenesis is potentially under more stringent selection than other phases of the life cycle in plants because cells undergo intense competition as haploids following the pollen development processes. Thus, the gene balance would be more critical in the highly sensitive meiosis stage. These data suggest that meiosis places exceptional demands on plant hormone signal transduction so that much higher selection pressure on appropriate gene balance results in the retention and expression of a greater proportion of duplicated genes in meiosis during plant reproduction.

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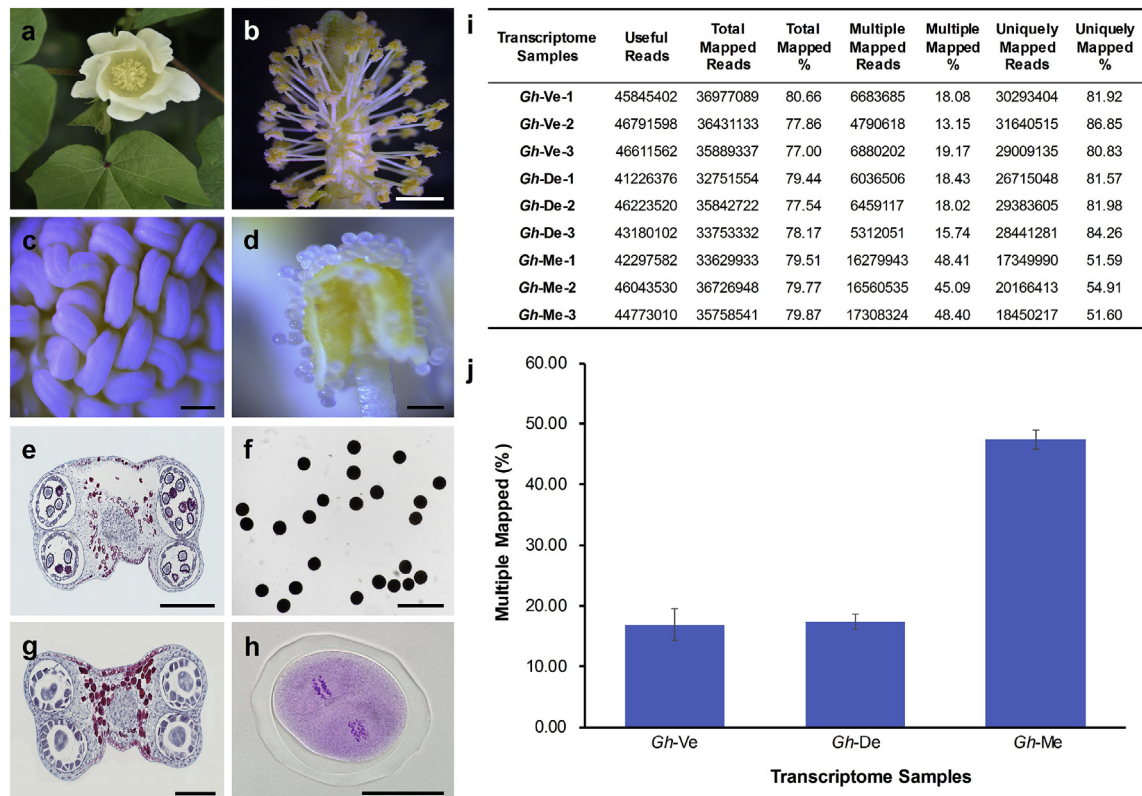


Fig. 1. Developmentally staged male gametophyte and meiosis-specific expression of duplicate genes in flowering cotton. **a** Blooming flower of angiosperm cotton. **b** Stamen in bloom, *Bar* = 5 mm **c** Undehiscent anther, *Bar* = 1 mm **d** Dehiscent anther in bloom, *Bar* = 500 μ m **e** Developed pollen staged anther histological section, *Bar* = 500 μ m **f** Fertility detection of developed pollen grains, *Bar* = 500 μ m **g** Meiosis staged anther histological section, *Bar* = 100 μ m **h** Meiosis staged microspore mother cell, *Bar* = 25 μ m **i** Statistics of multiple mapped duplicate genes from the transcriptomes. **j** Duplicate gene expression is significantly overrepresented in meiosis. Error bars denote SD of three biological replicates. **Gh**: *Gossypium hirsutum*, **Ve**: Vegetative tissue of shoot apex, **De**: Developed pollen stage, **Me**: Meiosis stage.

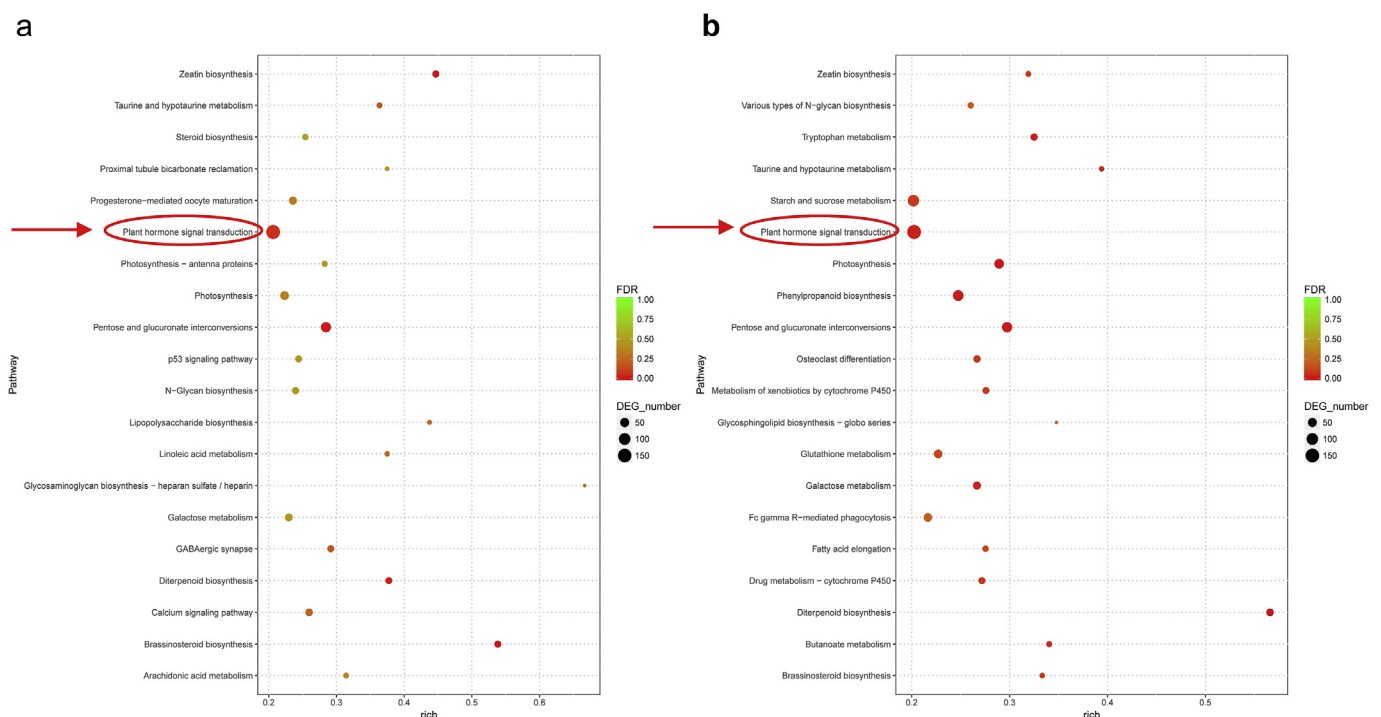


Fig. 2. KEGG pathway enrichment on meiosis-specific expressed duplicate genes. **a** Developed pollen versus meiosis stage. **b** Vegetative tissue versus meiosis stage. **FDR**: False Discovery Rate, corrected P-Value, **DEGs**: Differentially expressed genes.

The study in this letter provides direct evidence that suggests that meiosis during plant male gametogenesis is the master driver for gene duplication in angiosperms. These findings thus highlight the importance of meiosis to the evolution of gene duplication in higher plants and provide a significant opportunity for understanding the biological basis of the function and evolution of genome-wide duplicate genes.

3. Perspective

Understanding the contribution of plant gene duplication to evolution, ecology and agriculture is important in light of environmental challenges, including the old problems of diversity, adaptation and grain yield impacting food security, as well as new issues related to global climate change. Considering the critical role of meiosis in genetic variation and sexual reproduction in plants, the finding of the connection between the meiosis and gene duplication reported in this letter opens a new avenue to illustrating the impact of duplicated genes in meiosis on plant reproduction, as well as their ultimate evolutionary, ecological, and agronomic impacts.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.bbrc.2019.04.127>.

Transparency document

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